S. Subramanya
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FRIDAY GROUP'S

ANNUAL COLLOQUIM

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ABOUT THE GROUP

About a year ago:

When a group of confused students desperate to learn, but finding it difficult to digest the 'new' in ever-growing literature were fretting with their chins down, Reddy came out with a suggestion for starting a 'group discussion' to help each other. The suggestion was received and put into effect the next Wednesday (16-11-1983). That was the birth of the "Wednesday Group".

During the Year:

It grew as 'Wednesday Group' and matured as the 'Friday Group'. During this maturation, it attracted several students from different spheres, expanded its areas of interest and developed as a working group. Creditably enough the group survived against the odds of weak attendance and initial discouragement. It succeeded in triggering the minds of atleast a few amateurs to initiate work in new areas of research.

Today:

It is a group of enthusiastic youngsters with diverse interests. It is an un-inhibited school for learning new things, new ways of reading and dissecting literature and above all a source of confidence.

It is based on the belief of its constituent members that a student of biology knows no boundaries in science.

Next:

The group organised this workshop as an occasion, to celebrate the anniversary of the group and to expose others to its activities. It is also intended to welcome new-comers to the group to strengthen it further and to get help back from it.

"FRIDAY GROUP IS AN EXPERIMENT IN LEARNING"

SCIENTIFIC STERILITY IN MIDDLE AGE

Time-consuming, prestigious, nonscientific work
may lead to intellectual death at an early age

Perhaps half or more of all science Ph.D.'s move into research or teaching positions in minor or second-rate institutions, live lives of essential mediocrity, and continue until retirement to repeat and slightly extend the research work that got them their doctorates, but they never have any real hope or prospects of making anything but a miniscule addition to knowledge. The remainder constitute what I will call the scientific middle class. From them are recruited the staffs of first-rate institutions, editors of journals, speakers at symposia, officers of societies, recipients of most research funds, and from them come most of the "good" articles in scientific journals.

They progress in income and reputation from junior to senior positions, they are in good enough repute nationally so that they can hold their own in academic infighting and by the age of 35 to 40 they have tenure positions, growing children, half-paid mortgages, and an air of solidity, if not prosperity.

Most of the men of the scientific middle class enter on a period of relative sterility just when they have established their reputations and might have been expected to be at their most productive.

The typical problem of a middle class scientist seems to be that he has initially a certain fear of failure combined with the possibility that he really is another Einstein. The combination is enough to keep most graduate students working hard and productively.

Very pleasant milestones are encountered by every young scientist. His first clearly defined problem, first successful experiments, first oral presentation to a class or at a scientific meeting. Fellowships, assistantships and the vanishing of less effective classmates all give the student the sense that he is progressing. Reprints of his first published paper are sent to parents and grandparents; and the first reprint requests from strangers in Iowa or, better still, from agricultural stations in India or Brazil produce a tremendous elation. A brand new Ph.D. is ready to take on the work single-handed, and usually does, which accounts for the high mobility of college instructors.

Reprint requests are beginning to lose their spice when the first symposium invitation arrives, and for the next several years there is an almost visible swelling in stature both in and out of the home institution. The rate at which invitations arrive accelerates since the people who organize symposia are generally cautious men who invite only those speakers who have already demonstrated their competence as symposium participants.

Now the middle class scientist has arrived. He has relative affluence, and many props to his ego. All the fears and insecurities of the new Ph.D. are gone. To be sure, the work isn't as much fun as it had been. Hired technicians never do it quite right, but considering how much more he gets done, it is worth it.

We can't all be Einstein and we can't all do work; some of us must sacrifice ourselves, jet first-class, to lead the field, explain it to the others, popularize, write. And if our middle class scientist can believe that, he's dead already. If he hasn't read this far, the problem hasn't hit him yet.

It should be noted that, in one sense, fenetic activity does not stop scientific production. If a scientist is willing to keep turning the crank on the same machine that ground out his early research, he can be nominally productive for his entire life, but this is just another kind of death.

How do you stay scientifically alive ? The motivation of a scientist is basically curiosity, in most cases overlain with other things, and these other things (particularly money, prestige, and security) are so important early in a career that when they must disappear as motivation, if the curiosity is to survive, it is difficult to let them   Is there a recipe for preserving scientific clues without being either Einstein on one hand or a graduate student on the other ?

Some of our very good scientists, including Noble prizemen swtiched fields, thereby bringing their intellectual maturity to bear on completely fresh problems. It is almost surely the case that switching technique, approach, problem, or even species can prevent stagnation to some degree. Alteration in the teaching-research ratio may also help. An irrelevant question from an elementary student can, on occasion, be very stimulating, and conversely a year of isolation can counteract the comfortable adulation so freely given to histrionically gifted lecturers. But all of these solutions require that the research worker divest himself to at least some extent of smothering security.

Another kind of trap which normal scientific progress provides is the unexamined samples, the unanalyzed data, and the outdated or nonfunctional equipment that fill laboratories and file cabinets. We all know men who have become lost in the attic of research, always about to finish some yellowing heap of numbers or drawings or manuscript.

The implicit assumption is that if a scientist is freed of secondary problems, so that he is confronted with the choice of being bored or being creative, he will be creative.

(condensed from the same titled article
by Slobodkin, publishied in Scientific American.
1981,)

ENDOSPERM BALANCE NUMBER (EBN) HYPOTHESIS

S.P. DINESH KUMAR

Endosperm, a tissue peculiar to angiosperms, is formed by the fertilization of central cell of the embryo sac by a sperm identical to the one which fertilizes the egg. The endosperm is triploid (3X) in crosses between diploids (2X x 2X) since it receives two sets of maternal chromosomes and one set of paternal chromosomes. After fertilization, the endosperm grows rapidly, becoming the nutritive tissue for the embryo.

There are several types of endosperm dysfunctions which prevent success in **crossing programmes**. One type is evident in intraspecific, interploidy crosses. Lin[7] clarified the problem by demonstrating that in corn a 2:1 ratio of maternal:paternal chromosomes is necessary for normal endosperm development.

An "Endosperm Balance Number" (EBN) hypothesis has been proposed[4] to explain endosperm development in both interploidy intra-specific crosses in some of the Solanum Spp[6]. In this hypothesis the genome of each species is assigned an "effective ploidy" (or EBN) on the basis of its crossing behaviour to a standard species. It is the EBN which determines the effective ploidy in the endosperm of each species, and it is the EBNs which must be in a 2:1 maternal : paternal ratio (not necessarily the ploides).

The EBN hypothesis is an expansion of an "Endosperm Balance Factor Hypothesis" developed by Johnston and amplified by by den Nij's and Peloquin.

Further test of the EBN hypothesis has been conducted in potato[5], which indicated that the 2:1 EBN ratio is a necessary condition for successful endosperm development in interspecific crosses.

The EBN hypothesis also appears to clarify the results of interspecific crosses in several other genera including cotton[8], tomato[2] and Datura[1].

The EBN hypothesis also has evolutionary and genetic implications and helps in explaining the importance of :-

1. Isolating mechanism.
2. 2n gametes[3]
3. Disomic Inheritance
4. Reciprocal differences in interspecific crosses.

The EBN hypothesis is probably simplification of the solution. Certainly other interactions are also important in determining endosperm development. A 2:1 EBN ratio is necessary but not a sufficient criterian for the success of a cross.

The value of the EBN hypothesis, however is that it;

1) helps to predict the success of and resultant ploidy from interspecific crosses;
2) serves as a model for the incorporation of formerly inaccessible germplasm in crops where endosperm development is the barrier to successful hybridization;
3) adds coherence to the interpretation of the data on endosperm development in interspecific crosses;
4) points to the fundamental role of endosperm in evolution, and
5) focuses future work on the genetic and physiological factors which underline the EBNs.

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TRANSFORMATION IN PLANTS

T.V.Venkatesh.

Transformation of procaryotes by addition of exogenous genetic information has been possible since the classical experiments of Avery et al[1] and the demonstration that bacteria can take up and integrate DNA into their genome.

Until recently, such cell manipulations with higher organisms seemed almost impossible because of the inadequate means available for the critical studies. Nevertheless, DNA mediated corrections in higher organisms were reported[3] and such studies in plants were also reviewed[2].

The experiments of Ledoux et al[3]. on DNA mediated correction of nutritional mutants of Arabidopsis thallana will be discussed.

They treated seeds of A.thaliana with foreign DNA (of bacteria)and corrected the cells for thiamine deficiency. Arabidopsis is a small flowering plant with a duration of 30 days. They used mutant lines with leisons in the branched pathway for thiamine synthesis. These mutant lines were able to obtain maturity if they were fed with thiamine. But if thiamine was withheld, plants grown on mineral medium die within 15 to 20 days. Treating the ungerminated seeds during imbibition with a solution of appropriate bacterial DNA remedied this. From treated seeds few plants were obtained that grew satisfactorily without added thiamine. The observed frequency of correction was far higher than the spontaneous reversion rate and in any case the corrected plants could be distinguished phenotypically from normal plants without leisons for thiamine synthesis. The corrected plants were homozygous, and there was no segregation on selfing in the progenies of the corrected lines. All plants (F_1, F_2 and F_3) originating from each corrected plant looked phenotypically alike. Reciprocal crosses between corrected mutants showed that the correction could be transmitted through male as well as female, which excludes maternal (cytoplasmic) inheritance. It appears that the foreign DNA got covalently linked to the recipient material as double stranded material.

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PARASITIC DNA

B.R.Chaya

A novel view about DNA emerging nowadays is that particular sequences of DNA can be neutral, irrelevant, disposable or even parasitic. By parasitic it is meant that it apparently does no good to the organism and may be harmful, yet it can persist and spread. Its ecosystem is ultimately the cell genome itself. This has opened up some of the most taxing problems of evolutionary biology including the ways of speciation and origin of sex.

Parasitic sequences can be thought of as viruses inside genomes. Unlike viruses; they do not spread by infecting a cell, reproducing within and then escaping from the cell. Rather, they engage in 'duplicative transposition' wherein newly synthesized free floating copies are made from a copy located on a chromosome and then deposited at a new chromosomal site without loss of the original sequence. Such transposable elements will usually spread throughout a population unless their effects are extremely detrimental[3].

Orgel and Crick suggested[2] that the organisms whose genomes contain an excessive proportion of parasitic DNA would be at a metabolic disadvantage relative to organisms with less of parasitic DNA and so would be eliminated by a normal mechanism of natural selection. Thus we may expect that the mechanisms for the formation and deletion of non-specific DNA will adjust in each organism, so that the load of DNA is sufficiently small to avoid ~~producing~~ a large selective disadvantage. However, the elimination of a particular stretch of parasitic DNA may be a very slow process even in a geological time scale.

Hickey[1] proposed an explanation to the mechanism of evolution of sex. If some DNA sequences appear to evolve for no other end than ensuring their vertical transmission from generation to generation there could also be parasitic DNA sequences which foster their transmission horizontally between lineages. This can be achieved by establishing genetic exchange between host organisms; the DNA could infect new hosts as a result of the genetic exchange. Sex thus becomes a means of genetic contagion for these parasitic sequences. There are sequences which do just this, like the 'F' factor of E.coli, mating type controlled by transposon in yeast and M-factor responsible for maleness in Dipteran insects. Thus sex might have originated as a result of selection acting on parasitic DNA to foster horizontal transmission between host cells. However, it is difficult to explain how females get benefit, evolutionarily, by getting fertilized by males. May be that it is difficult for them to escape mating evolutionarily. In this context, males can be seen as parasitic DNA made manifest at the organismal level.

It has been felt that this parasitic DNA serves the purpose of 'padding' if useful DNA is too little to have selective advantage. However, this does not explain the large amounts (70 % of total DNA) of parasitic DNA present in higher organisms.

Much more information is required to decide whether the parasitic DNA has a role in deciding life style or duration of meiosis or increase in the cell per nuclear size etc.

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BIOENERGETIC CONSIDERATIONS IN CERAL BREEDING FOR PROTEIN IMPROVEMENT

S.G.Hegde.

In plant breeding programmes, considerable emphasis is being placed on improving the nutritional quality of cereals by increasing the protein concentration and altering the protein composition in grains to ameliorate the balance of lysine and other limiting aminoacids. A major problem in such programmes is combining high grain yield with increased or nutritionally-better grain proteins. Numerous observations indicate that the grain protein concentration is inversly correlated with yield in cerelas[1]. The underlying basis for this relationship has not been clearly enunciated. The fact that the gross energy in the dry matter of high protein grains is higher than in low protein grains[2], and that this energy differential has to be provided by the plant producing the grain, appears to have been neglected. To understand the situation better an examination of the energitics of grain production is essential.

Sinclair and de Wit[3] considered seed biomass yield and the nitrogen requirement in 24 different crops with seed protein concentrations varying from 8 to 38 percent. Their study included cereals, pulses and oilseeds. They inferred that in any species simultaneous increase in grain protein concentration and yield are incompatible from energetic point of view. To achieve both increments there is competetion, not only for the available carbon skeletons but also for the energy derived from photosynthates.

The synthesis of more protein or more carbohydrates in the developing grain demands additional photosynthates; increment in nitrogen input for additional protein and more efficient utilization of assimilates towards grain production may help achieve the desired results.

Purpose of this paper is to direct the attention of plant breeders and others to consider the above said problems while breeding for altered nutritional composition of grain. These considerations will be of practical value when the genetic potential of the plant for energy conversion is expressed. This can be obtained only under favourable environments with the essential supplementary inputs.

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* * *

SWOLLEN-THORN ACACIAS AND THEIR ANT GUESTS-COEVOLUTION?

V.V.Belavadi

The interdependency between swollen-thorn acacias (STA) and their ant inhabitants has been shown to be a case of mutualism[2,3]. In this species pair* (*Acacia cornigera* and *Pseudomyrmex ferruginea*), the ant is dependent upon the acacia plant for food and shelter, and the plant upon the ant for protection.

All obligate Acacia ants (OAA) in the New World tropics belong to the genus *Pseudomyrmex* (However, not all species of the genus have such relationship). Further, these OAA are not specific to any one species of STA, but for the STA-like form. These ants are essentially restricted to central America (below 1500m).

THE ANT X ACACIA INTERACTION: The ant: A newly emerged and mated queen ant finds an unoccupied seedling or sucker shoot of a STA. She gets into a green swollen thorn by cutting an entrance hole and lays eggs inside. She forages nector from foliar nectaries for herself and harvests beltian bodies for its larvae. As the colony grows it occupies all the thorns of the plant with upto 25 percent of the workers normally active on the plant at any time of the day. About nine months of colony growth is necessary to produce enough of workers to patrol the entire outer surface of the STA in an effective and aggressive manner (Colonies may grow to contain as many as 1600 workers in three years, sometimes one colony might inhabit several trees within 3 to 10 meters).

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*Though there are over five species of *Acacia* and *Pseudomyrmex*, while explaining the phenomenon more emphasis is laid on these two species.

With a few notable exceptions, the workers attack any other insects on the acacia and drive them off by biting and stinging. They also attack any living plant (other than another STA), which touches STA's foliage or grows in an area of 10 to 150 cm(dia) below the acacia. Thus the acacia grows in a cylindrical space free of other plants and pests. The efficiency of the protection given to STA is a function of workers aggression and patrolling consistancy which further depends on colony size, air temperature and food availability.

THE PLANT: The young STA grows from a seed or a stump left by fire, flood or a land clearing. As it grows, during the first 9 to 24 months, without being occupied (by OAA), it is subject to insect and rodent attack which greatly reduce the already small populations of young acacias. During this stage, a seedling progressively produces larger thorns, more leaflets with a special structure called beltian bodies and larger foliar nectaries, and such plants will be sooner or later occupied by OAA. Once occupied the acacia grows rapidly.

THE THORNS: The stipules (thorns) of STA are long, persistant (2-4 years). The total internal volume (of thorns) in a STA canopy will be about 100-800 cc. The thorn walls are waterproof and somewhat resistant to sudden increase in temperature. (In case of forest fires, even though the shoot is killed, the OAA colony may survive).

The Beltian body: Only STA have the tips of their leaflets modified into "Beltian bodies" (Thomas Belt discovered this in 1874). Beltian bodies are constrictions at the tips of leaflets gland like in appearance but not glands. These are rich in proteins and vitamins. Beltian bodies are unique botanically as they represent no preadaptation by the STA and there are no analogues in other legumes. The only clue to their origin lies in undescribed species of Eastern Costa-Rican acacia which may be regarded as the prototype. Some plants of this species have leaflets with a small clear apical portion[3].

The foliar nectaries: Nectaries on the upperside of the rachis are universal in all acacias[1,2]. The foliar nectaries of STA are much larger and much heavier nectar flow (The nectar mainly contains glucose and fructose), which is virtually the only sugar source for the OAA colony.

THE COEVOLUTION: The coevolution of an ant x acacia mutualistic interaction appears to be the product of an evolutionary feedback system par-excellence. There might have had been a multiplicity of changes in the STA which resulted directly in an increase in density or 'healthiness' of the occupant ants and indirectly in selection for the acacia genotypes which possess the changes. Like-wise, changes in the ant that resulted in the increase in reproductive capacity of the acacias might have effected selection for the *Pseudomyrmex* genotype which exhibited the changes.

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DIFFERENT METHODS OF BREAKING SELF-INCOMPATIBILITY IN Brassica oleracea.L.

T. JYOTHI

Like in any other crop, hybrids are important even in cole crops. For developing and maintaining inbred parent lines in production of hybrids self-incompatability (SI), a barrier, has to be broken. This can be done by several methods but bud pollination is being widely used in self-seed production at commercial level. Since it is time and labour consuming there is a need for much easier method. So, some techniques like steel brush pollination (SBP)[2], Electric aided pollination (EAP)[1] and Thermal aided pollination (TAP)[4] were tried.

In SBP method, a brush with hairs replaced by thin steel wires (0.1mm thick and 4mm long) were used for mutilating. Open flowers of different SI clones were pollinated with their own pollen for every 3 - 4 days. The ripe anthers were touched with the steel brush and subsequently stigma was damaged by pricking by steel hairs with pollen attached to it. Though the number of seeds per pollinated flower was same in this method and bud pollination, it would, presumably have been higher with daily pollination.

In EAP[3] anthers were held between insulated tweezers. During pollination the flower stalk was entwined with a wire near the flower to be pollinated, the other end was connected to the negative electrode. The insulated tweezers holding an anther were connected to the positive electrode. At the moment of brushing pollen on the stigma, 100 V current was passed for 2-3 sec. The number of seeds per flower was comparatively higher. The heat generated during the transit of current at the site of pollination might be the cause for breaking SI, since it was revealed that during EAP the papillae at the site of touch used to collapse.

A small soldering iron was modified in such a way that the temperature could be adjusted to 60, 70 and 80°C in TAP method, and this method showed markedly increased seed set.

It was assumed that during the application of these pollination techniques (EAP and TAP), the pellicle which is a waxy layer ensheathing the papillae, temporarily melted or softened. This short physical change apparently disturbed its sporophytic SI code with the consequence that that pollen showed a compatible behaviour. The switch from SI to self-compatible pollen behaviour was presumably not due to local removal of the pellicle because by this procedure tube penetration was totally prevented.

Thus, very probably application of radiation, heat disturbs or changes SI code of the pellicle, by denaturing the S-specific proteins.

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PHYLETIC SIZE INCREASE - AN ANALYSIS

R. UMA SHAANKER

Cope's rule is the name customarily applied to the widespread tendency of animal groups to evolve toward larger physical size. Larger species tend to appear later in a group's phylogeny. This is a historical pattern with considerable empirical support in the fossil record.

Newell[2] demonstrated phyletic increase in size for a variety of lower organisms, including echinoderms, corals, brachiopods, molluscs and foraminiferans (bottom-dwelling, marine protozoa).

Evolutionary theory does not lack explanation for this trend. Most argue a selective advantage to large size. For example, large animals, it is suggested, have greater control over the effects of their environment and are therefore less likely to suffer predation, desiccation, heating, cooling and starvation[6]. Rensch[3] argued that larger species are more mobile and have greater visual power, higher fecundity, larger individual offspring, increased capacity to learn and increased morphological specialization. Admittedly, some of these advantages are debatable. For example, large animals have fewer prey, they may suffer high levels of parasitization. Most positive advantages in large body size are offset by compensating disadvantages and the principles of similitude suggest that large and small animals normally perform equally well. As Gould[1] suggested, the continued existence of both large and small species argues that both are viable strategies.

In 1973, Stanley[4] rephrased Cope's rule. Rather than ask why many phylogenetic trees evolve toward large species, he asked why many trees begin at a relatively small size. On re-examination of the data, he found that though maximum sizes do increase with evolution the mean and median remain unaffected. This argues against a general selective advantage for larger size. The question then is why so few species become large ?.

Available size frequency distribution for modern as well as extinct taxa suggests that small species are overwhelmingly abundant. Stanley[4] following Rensch[3] suggested that the left-handed tail of these distributions is normally truncated, because some irreducibly small feature sets a lower limit for each basic animal body plan; an insect head capsule must always be large enough to hold a neuron. The limitation of the right-hand tail are less sharp so this tail tends to extend over time, which is why we recover few large species. However, these tend to be an evolutionary blind alley. They become poor potential ancestors.

A number of traits ensure that small species are likely to produce new evolutionary trees. Small species are more easily isolated geographically because they have smaller geographic ranges[7], smaller home ranges and lower mobilities. Further, if species biomass is unaffected by species size, small species produce more offspring (r_m). Their offspring will also be more heterogeneous genetically.

On the other hand, large species evolve more slowly because of their low rates of speciation and high rates of extinctions[5]. Evolution thus seems to have favoured smaller species, and large size tends to be an evolutionary dead end. Because evolutionary arguments are normally couched in causal terms, the foregoing points should lend support to the arguments based on the size frequency distributions of modern and fossil faunas.

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GENE TRANSFER USING IRRADIATED POLLEN.

N.D. DASHARATHA RAO.

The most common method of combining genes from two organisms is by sexual hybridization. But elimination of accompanying undesirable characters normally require several generations of back crossing and selection which may greatly prolong the breeding period depending on the nature of gene action controlling the character[2]. However, a variety can often be improved considerably by introducing only one or a small number of specific genes. Hence Jinks *et al.*[1] attempted a combination of sexual hybridization and irradiation to transfer genes more rapidly in *Nicotiana rustica* (2n=48).

When heavily irradiated pollen from a variety was used as the inducer on a contrasting variety acting as maternal parent, even though the progeny resembled the maternal parent to a large extent they were not true metromorphs (diploid parthenogenesis is called matromorphy, the plants developed by matromorphy are called matromorphs[3,4]) because they usually have at least one character of the paternal parent.

At the highest dose of gamma irradiation (20 krads) the progeny received only one or sample of many heritable characters from the paternal parent. By selecting within the progenies, isolation of the pure breeding material variety but specific characters transferred from the paternal parent could be achieved To achieve the same end by conventional means would require a combination of many generations of recurrent backcrossing and selection.

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INDUCING VARIABILITY BY PROTOPLAST CULTURE

K.S.MURALI

Genetic variability among plants regenerated from cell culture (somaclonal variation) appears to be an uniquitous phenomenon. It is a source of useful variability for plant improvement. In an attempt to use this somaclonal variation as a source to derive disease resistant plants Than tong et al.[3] succeeded in getting resistant plants.

Protoplast derived calluses of tobacco (Nicotiana tabaccum cv. 'Samsun') were selected for their resistance to toxins from Pseudomonas syringae Rpv.tabacci, which causes wildfire disease, and from Alternaria alternata pathotype tobacco, which causes brown spot. A number of plants were generated from each of the toxin-selected protoplast-derived calluses. A large percentage of the plants obtained from the second cycle calluses were resistant to infection by these pathogens. Resistance to wild fire disease, however, seems to be unrelated to resistance to brown spot disease. Variations in the morphological characteristics of the regenerated plants were found. Results of an assay of the Regeneration indicate that the resistance shown by R_o plants against both diseases is heritable.

In an attempt to attribute causes for the somaclonal variation Santos and Hardo[2] reported that ploidy level of the regenerated calluses will result in the variability. The descriminant analysis of the chloroplast number, leaf length/width ratio and petal length showed that discrimination among callus-derived cells was due to ploidy levels. The genetic events that give rise to somaclonal variation are not yet understood, while aneuploidy seems not to be a major contributing factor, meiotic analysis of regenerated plants has revealed extensive chromosomal rearrangements such as translocations, inversions, subchromatid exchanges & partial chromosomal loss.

Lorz and Scowcraft[1] determined the effect of cell culture duration, sub-optimal (stressed) growth conditions, and chemical mutagenesis on somaclonal variation and demonstrated the cell culture which causes change which persists in adult plant and perturb the segregation ratio.

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WHY AN ELEPHANT FORAGES BAMBOO-WHILE RABBIT DOESN'T ?

T.Veena.

The explanations of proportionality changes in morphology and accompanying changes in physiological rates are often rooted in geometric solutions to animal design[2,3]. A number of physical parameters related to body weight are changing at concert but at different rates[2]; as a result animals will show structural, behavioural and functional responses to body size changes. Metabolic rate is one such parameter. If rate of metabolism determines the nutritional requirements and gut size determines the capacity to process food into nutrition, then non linear response of metabolism coupled with the linear response of gut size produces much higher ratios of metabolism to processing capacity in small animals relative to large animals[1,4]. This statement is strengthened more formally by comparing the retention time or passage time of food in gastrointestinal tract in small animals and large animals. This is based on the fact that plant material is homogenous in its response to the digestive system. But it is not so in nature, because foraging behaviour of herbivores indicates that the fibre component of diet increases more rapidly with increasing body size. This fibre in diet ultimately correlates with the distribution of biomass of plants which increases with its increasing fibre percentage. From the foregoing it is obvious that Elephant which has longer retention time and delayed passage rate consumes high fibre containing bamboo, while Rabbit eats lucerne containing less fibre.

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POLLEN - A RICH SOURCE OF VARIABILITY ?

P. S. BALAKRISHNA

Mutation breeding has become a fashion rather than a necessity - an observation which needs consideration. There is a large amount of variability existing in the form of uncollected, available but yet - to - be realized germplasm. Even though spectacular achievements have been made by exploiting germplasm (e.g., dwarf gene) and mutation breeding (Aruna castor, amber wheat) many a time success by these methods remains more like a mirage. So do we have some other source of variability to exploit ? The following review suggests that pollen grains possess large amounts of variability and we have only to uncover it.

Way back in 1920's[1] it was observed that the actual variability in pollen grains was higher by 12 times than adult variability. In a later experiment it was reported[2], that, while 'hybrid - lines' obtained from pollination by large quantities of pollen continued their usual seggregation, some other 'hybrid-lines' obtained from pollination by limited pollen grains were stabilized ie., seggregation was not found.

It is also a well known fact that pollen tubes growing along the flower pistil enter into competitive relations and only a few of them succeed in fertilizing the ovule[3], hence pollen grains of a flower differ among themselves. So it is possible that pollen from a single plant can be tested against wide range of stress conditions and this has been successfully demonstrated by identifying a cold resistant line through pollen selection.

An interesting paper [4] about how variability was uncovered by limited pollination will be presented. When lesser amount of pollen than ovule number was placed (in cotton, inbred over several generations) the bolls obtained out of this treatment was much heavier than the normally pollinated ones. The seeds (of the heavier boll) gave rise to plants which very much differed from the control and among themselves. One of the plants gave 200 % more yield than the normal. Moreover this high yielding ability remained unchanged in further generations. But how could this happen ? Two hypothesis have been proposed - 1. Mutation hypothesis and 2. Zygotic reprogramming to explain this singular phenomenon to some extent.

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OUTBREEDING DEPRESSION AND OPTIMAL OUTCROSSING DISTANCE

S. CHIDANANDA

Natural selection in sexually reproducing plants should often favour matings between individuals of intermediate genetic similarity. This helps to increase the fitness of its own type. Matings between very similar individuals may lead to inbreeding depression because segregational load is revealed, while matings between very dissimilar individuals may disrupt the locally adaptive combinations of genes, a phenomenon referred to as "outbreeding depression"[2]. This outbreeding depression is more conspicuous in plants subject to restricted pollen and seed dispersal. Such plants are likely to show pronounced microgeographic genetic differentiation resulting from drift in subpopulations isolated by distance or from adaptation to local edaphic and biotic conditions. Under these conditions short outcrossing distance may be optimal not only because of intra-genotype effects, but also because it produces offspring sufficiently similar to the female parent to grow successfully near her, yet sufficiently genotypically diverse to maximise the success of total progeny. The superior and specific agronomic characteristic demands programmes for seed production which insure the retention of genetic purity and prevention of inter breeding. Isolation by distance is a prime method of safeguarding the genetic purity of strains[1].

Price and Waser[2] experimentally determined under field conditions, the optimal outcrossing distance in several populations of Delphinium nelsoni, herbaceous perennial. They have chosen the pollen donor flowers either from the same plant (self pollination) or from plants at 1, 10, 100 or 1000m distance. For all hand pollination experiments mean seed set per flower were highest with and intermediate outcrossing distance and declined significantly at longer and shorter distances. In general they found that seed set was highest when pollen was transferred by hand over an intermediate distance of about 10m, This optimal outcrossing distance was also confirmed by the seedling survivorship. Matings between close neighbouring plants had reduced seed set, probably as a result of inbreeding depression. Matings between distant plants (pollen was carried by hand up to 1000m) likewise resulted in reduced seed set perhaps resulting from disruption of locally adaptive combinations of genes. They also estimated the extent of pollen flow in the D.nelsoni populations by measuring the plant-to-plant distances flown by the main pollinators, two species each of bumble bees and humming birds. A second estimate was made by examining the dispersal of floroscent pigments. The mean pollen flow distance using these methods was estimated as 1m. This discrepency, between pollen dispersal and optimal outcrossing distance, implied is most intuititvely pleasing that selection is expected to act on the plants such that pollen flow is increased so that mean pollen dispersal distance matches the optimal outcrossing distance. This actual pollen can be expected to reflect conflicting selection of plants to maximise amounts of pollen received as well as to optimise transfer distances or on plants to donate as well as receive pollen over optimal distances or on pollinators to minimise flight distances.

Local genetic differentiation, which may lead to outbreeding depression, may result from genetic drift caused by isolation by distance coupled with local selection for genetic coadaptation or from spatially variable selection in a heterogeneous environment. If pollen flow is increased the zone of genetic coadaptation increases in size and the zone of outbreeding depression is moved farther away. The optimal outcrossing distance is not stationary since it is determined by the areas of inbreeding and outbreeding depression[3].

In a heterogeneous environment different local selective pressure result in different locally coadapted gene complexes. When pollen flow is increased, it narrows down the range of optimal outcrossing distances.

Under an isolation-by-distance model of genetic differentiation, spatial distance and genetic correlation between individuals or populations are expected to be negatively related, that is greater the distance smaller the genetic correlation. This is experimentally determined in the plant Liatris cylindracea Michx, obtained by a genetic distance analysis of gene frequencies at 27 allozyme loci. Genetic distance is an index for measuring the accumulated number of gene differences per locus between groups of organisms. This analysis revealed genetic differentiation across very small distances and demonstrated that a restriction of gene flow has a profound effect on the spatial distribution of alleles within a population. Genetic divergence over distance appears to be a function of random gene frequency fluctuations. Genetic distance is positively related to spatial distance. This relationship is as predicted for a population in which gene dispersal is limited and genetic differentiation results from isolation by distance.

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RECOMBINATION IN INTERSPECIFIC CROSSES

P. GOPALA REDDY.

Breeders will be very often resorting to interspecific crosses to combine the desirable characters of two or more species, but many a time fail to realise the desirable variability in F_2 generation. In order to answer their failures Anderson[1] carried out an experiment.

~~The~~ Two species of Nicotinna (Nicotiana alata and N.langsdorffii) which produce fairly fertile hybrids, differing in four quantitative characters (corolla color, corolla tube length, limb width and lobing of limb) that are less affected by environmental factors were chosen.

The F_2 recombination of tube length and limb width, tube length and degree of lobing, limb width and degree of lobing and corolla length and style length showed that in all these cases there was no free recombination of the parental types. Instead, recombination was found to be restricted to a narrow segment of the total, running from combinations more or less like one parent through combinations of F_1 to combinations more or less like the other parent.

The author developed a mathematical formula for generalizing the results obtained. From this formula it was estimated that the actual character recombinations of the $F_{2,3}$ were less than 1/64th of the total possible recombinations.

In the light of these results, the known hindrances to character combination were discussed under the following headings; (a) Gametic elimination, (b) Zygotic elimination,

(c) Pleotropism and (d) Linkage. Evidence was brought forward to show that all these operated to hinder recombination in the above cross.

The hindrances imposed by linkage of multiple factor characters were found to be severe. It was shown that if the number of genes for each of such characters is large then all the polygene characters of an organism will be tightly linked with each other, and hence imposing severe restrictions on free recombination.

Theoritical considerations therefore lead to the same conclusion as did the actual data. Recombination in crosses between species and races was limited in the second generation to a relatively insignificant fraction of total recombination.

The limitations of F_2 character recombination were shown to impose a severe handicap and methods were described for selecting the most efficient parents for further breeding among the F_2's. The application of these conclusions to practical breeding problems will be discussed.

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ON MASS EXTINCTIONS

K. N. Ganeshaiah...

A recent analysis of the paleantological data for the past 250 M Yrs[2] has shown that the rate of extinction which has been declining has repeatedly shown sudden surges above the average rates.

Raup and Sepkoski[2] provided evidence to indicate that these sudden mass extinctions follow approximate cyclicity. Though doubts still persist about the duration of the phase interval between such two consecutive mass extinctions it has been generally shown to be around 30 M Yrs with a standard deviation of ±9 M Yrs. Since no terrestrial event can be sought to generate satisfactory explanation to this cyclicity Rampino and Stothers[3] have resorted to explain this by a galactic event. They show that this terrestrial cycle of mass extinctions is strongly correlated with the time needed for the solar system to oscillate vertically about the plane of the galaxy which is 33±3 M Yrs. This passing of the solar system through the galactic plane, they argue, results in collisions of solar system with intermediate sized to large sized inter-stellar clouds of gas dust which are sufficiently concentrated towards the galactic plane. This creates a gravitational perturbation in the comet family around the solar system and thereby increases the flux of comets and their residues near the earth leading to large body impacts. The consequences of this impact may be severe and widely ranging like increased radiation and temperature causing enhanced extinctions. In support of this is the evidence of iridium deposition corresponding to one of the recent mass extinctions involving the disappearance of the Dinosaurs about 65 M Yrs ago.

While another group[4] also came out with a similar explanation, Whitmire and Jackson[5] show that the existence of a distant solar companion star which approaches the solar system once in about every same time corresponding to the cycling period of mass extinction may also bring about such disturbance through the same phenomenon of comet impact following the gravitational perturbation of the comet family.

Whether Nemesis existed or not, whether companion star exists or not, mass extinctions continue to recur due to one or the other reason---------and what if it is true---------our fate ? "Sambhavami Ughe--Ughe-----?"

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TOPICS DISCUSSED IN GROUP

Sl.No.	TOPIC	SPEAKER
1.	Artificial sweetners.	Asha Javalogi
2.	Pollen:a rich source of variability ?	Balakrishna, P.S.
3.	Genetic Programme of cell death.	-"-
4.	Ant-Accacia co-evolution	Belavadi, V.V.
5.	Facilitation as a means of succession	Chaya, B.R.
6.	Parasitic DNA	-"-
7.	Temperature sensitive male sterile mutant in Tomato	Chidananda, S
8.	Outbreeding depression and optimal out crossing distance.	-"-
9.	Costs and benefits of flower abscission & fruit abortion in Asclepias speciosa	-"-
10.	Gene transfer using irradiated pollen	Dasha ratha Rao N.D.
11.	Endosperm Balance Number(EBN)hypothesis	Dinesh Kumar. S.P.
12.	Role of correalations in plant breeding.	Ganeshaiah, K.N.
13.	Does Pollen grain to ovule ratio dep-ends upon the pollination efficiency.	-"-
14.	On Mass Extinctions.	-"-
15.	Skewed distribution of plant weights and self thinning phenomenon.	-"-
16.	Induction of heriditary changes in capsicum through ordinary grafting.	Gopal Reddy.P.
17.	How to produce a human being with three chromosomes.	-"-
18.	Gynodioecy as a a possible strategy in survival.	-"-
19.	Recombination in interspecific crosses.	-"-
20.	Gene flow.	Hegde, S.G.
21.	Bioenergetic consideration for protein improvement in cereals	-"-

22.	Cross sterility in Sorghum.	Hegde. S.G.
23.	Genetic control of *Heliothis armigera*.	Jyothi.T.
24.	Different methods of breaking self incompatability in *Brassica oleraceae*.	
25.	Production of F_1 hybrids from ethrel induced male sterility in *Brassica juncea*.	Krishnappa
26.	Inducing variability through protoplast culture.	Murali.K.S.
27.	Population structures and out crossing rates.	-"-
28.	Ecology of fruit and seed production in *Cassia fistula*	-"-
29.	Dominance and suppression in competing mono cultures.	-"-
30.	Evolution of Gynodioecy in Plants.	Paramesh.C.V.
31.	The cell electric	-"-
32.	Physiological evolution of angiosperm pollen.	Swamy.M.
33.	Body size, life history and ecology.	Uma Shankar, R.
34.	Body size, Home ranges in animals.	-"-
35.	Natural selection and Michale's constant.	-"-
36.	Feeding ecology in Herbivorus animals.	Veena.T.
37.	Diets of prehistoric people.	-"-
38.	Parent - offspring conflict.	-"-
39.	Characterization of Adult plant resistance to *Erysiphe graminis* in barley.	Venkatesh.T.V.
40.	Transformation in plants.	-"-
41.	Theoretical resistance model	-"-

Michaelis constant and its evolutionary implications

R. UMA SHAANKER

In 1913, a major breakthrough in our understanding of the kinetics of enzyme catalysed reaction was provided by two Scientists, Michaelis and Menten. They gave an expression,

$$V_o = \frac{Vmax\ (S)}{Km + (S)}$$

which related the initial velocity of the enzyme catalysed reaction (V_o) to the maximal velocity attained (V_{max}) and the substrate concentration(S). An important fall-out of this equation however, was the lumped constant K_m or the Michaelis - Menten constant. This constant indicated the substrate concentration when $V_o = \frac{1}{2} V_{max}$. Translating it into its biological functional sense, it indicated the affinity of enzymes to bind substrate molecules.

It was found by Crowley (1975) that this system of equations, with the parameters Km and Vmax could usefully explain the kinetics of many other relationships as well, namely, the rate of nutrient uptake versus nutrient concentration, prey capture rate versus prey density or the c carbon assimilation rate versus light intensity. Further, since Km of a given relation is also a species constant, it was suggested by Crowley (1975) that the Km's must have undergone stringent selection by natural selection process.

In this paper, while discussing Crowley's work, I explore further the implications of Km and consider how it might be related to the metabolic rate and the intrinsic multiplication rate or the Malthusian parameter.

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